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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:09:27 ; Search time 8498.8 Seconds
(without alignments)
30.345 Million cell updates/sec

Title: US-09-851-670-16

Perfect score: 24

Sequence: 1 gtccaaaggagagaatttctgca 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched:

Total number of hits satisfying chosen parameters: 111874

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

EST:*

1: em_estfun:*

2: em_esthum:*

3: em_estin:*

4: em_eston:*

5: em_estpi:*

6: em_estba:*

7: em_estro:*

8: em_estov:*

9: em_htc:*

10: gb_est1:*

11: gb_est2:*

12: gb_htc:*

13: gb_gss:*

14: em_gss_fun:*

15: em_gss_hum:*

16: em_gss_inv:*

17: em_gss_pln:*

18: em_gss_pro:*

19: em_gss_rnd:*

20: em_gss_vrt:*

21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.8	65.8	51	13 A2793014	A2793014 51 bp DNA DEFINITION 2M0045E17R Mouse 2M0045E17R Mouse plasmid library clone UGGC2h40045E17 R. DNA sequence.
2	15.2	63.3	59	13 A2793014	A2793014 51 bp DNA DEFINITION 2M0045E17R Mouse 2M0045E17R Mouse plasmid library clone UGGC2h40045E17 R. DNA sequence.
3	14.4	60.0	54	13 A2793014	A2793014 51 bp DNA DEFINITION 2M0045E17R Mouse 2M0045E17R Mouse plasmid library clone UGGC2h40045E17 R. DNA sequence.
4	14	58.3	39	11 BF339449	BF339449 602039103 602012848
5	14	58.3	39	11 BF342032	BF342032 602012848
6	13.8	57.5	29	13 A2658555	A2658555 1M035113
7	13.8	57.5	39	10 AU011691	AU011691 AU011691
8	13.4	55.8	43	13 A2869134	A2869134 2M0181E10
9	13.4	55.8	51	10 AU013478	AU013478 AU013478
10	13.2	55.0	29	13 A2868457	A2868457 1M0396L17
11	13.2	55.0	42	13 A2632296	A2632296 1M0487E12
12	13.2	55.0	57	10 AU595919	AU595919 AU595919

ALIGNMENTS

RESULT	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
A2793014	A2793014	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenem,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss University of Utah Genome Center
					Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
					84112, USA
					tel: 801 585 5606
					fax: 801 585 7177
					email: ddunn@genetics.utah.edu
					Insert length: 10000 Std Error: 0.00
					Plate: 0045 row: E column: 17
					Seq primer: CACAGGAGAACAGCTATGACC
					Class: Plasmid ends
					High quality sequence stop: 51.
					Location/Qualifiers
					1. .51

AUTHORS	Dunn, D., Avragi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ismail, H., Longacre, S., Mahmood, M., Meeden, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dunnagenetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0535 row: 1 column: 13 Seq primer: CGTTGTTAAACGACGGCAGT Class: Plasmid ends
FEATURES	High quality sequence stop: 29. Location/Qualifiers
source	1. .29
	/organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGCIM0535113" /clone_l1b="Mouse 10kb plasmid UGGC1M library" /sex="Male" /lab_host="E. coli strain X110-Gold, Tr-resitant, F-" /note="Vector: PWD454n. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://wwwjax.org/resources/documents/snars/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (914732141gb) AF129072.1, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT	5 a 5 c 8 g 11 t
ORIGIN	
RESULT	7
Query Match	57.5%; Score 13.8; DB 13; length 29;
Best Local Similarity	88.2%; Pred. No. 4 2e+04;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Y	2 tccaaaggcagaatt 18
b	29 TCCTAGCCAGCAATT 13
AU011691/c	
OCUS	39 bp mRNA EST
DEFINITION	AU011691 Schizosaccharomyces pombe late log phase cDNA
CESSION	Schizosaccharomyces pombe cDNA clone spcl1857, mRNA sequence.
VERSION	AU011691
EWORDS	AU011691.1 GI:3356600
EST.	fission yeast.
OURCE	Schizosaccharomyces pombe
ORGANISM	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomyctaceae;

purified. The sheared, adaptored mouse DNA was annealed to purified vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 9 c 5 g 10 t
ORIGIN

Query Match 55.0%; Score 13.2; DB 13; Length 29;
Best Local Similarity 83.3%; Pred. No. 7.7e-04;
Matches 15; Conservative 0; Mismatches 3;
Indels 0; Gaps 0;
Qy 6 aggcagagaaattctgc 23
Db 29 AGGANGGCAATTICAGC 12

RESULT 11

AZ332796/c
Locus A2632796 42 bp DNA GSS 13-DEC-2000
Definition IM0487E12R Mouse 10kb plasmid UGGC1M library Mus musculus genomic
Accession A2632796
Version A2632796.1 GI:11754986
Keywords GSS
Source house mouse.
Organism Mus musculus

Reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Authors Dunn,D., Aoyagi,A., Barber,M., Beaumont,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenah,E., Pedersen,T., Reilly,
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
Title Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Journal Unpublished (2000)
Comment Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
tel: 801 585 5606
fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0487 row: E column: 12
Seq primer: CACACAGGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 42.

FEATURES source
1. .42
/Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0487E12"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42mv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (gi|4721149|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT

8 a 5 c 8 g 21 t
ORIGIN

Query Match 55.0%; Score 13.2; DB 13; Length 42;
Best Local Similarity 83.3%; Pred. No. 7.8e+04;
Matches 15; Conservative 0; Mismatches 3;
Indels 0; Gaps 0;
Qy 2 tcacaggcagacaattt 19
Db 28 TCCAGGCAAGACATT 11

RESULT 12

A2632796/c
Locus A2632796 57 bp mRNA EST 30-JUL-2001
Definition mRNA sequence.
Accession A2632796
Version A2632796.1 GI:15007994
Keywords EST
Source Silurana tropicalis
Organism Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Xenopodinae; Silurana.
Authors (basses 1 to 57)
Huckle,E., Taylor,R., McMurray,A., Ashurst,J.L., Zorn,A.M. and
Roger,J.
Title Silurana Xenopus tropicalis EST project 2001
Journal Unpublished (2001)
Comment Contact: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropessanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGes004019.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers

FEATURES source
1. .57
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TGes004019"
/clone.lib="XGC-gastrula"
/dev_stage="gastrula (stages 10-5-13 mixed)"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCSI07; Site.1: EcoRI; Site.2: NotI; cDNA
was oligo dT primed from 5'ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCSI07 with EcoRI at the 5' end and NotI at the 3'
end."
ORIGIN

BASE COUNT

11 a 28 c 10 g 8 t
ORIGIN

Query Match 55.0%; Score 13.2; DB 10; Length 57;
Best Local Similarity 83.3%; Pred. No. 7.9e+04;
Matches 15; Conservative 0; Mismatches 3;
Indels 0; Gaps 0;
Qy 7 ggccagagaaattctgc 24
Db 56 GGCAGGGCAATCTCGCA 39

RESULT 13

AUT05510

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